

1646

RAW SEQUENCE LISTING DATE: 11/28/2000
PATENT APPLICATION: US/08/900,220C TIME: 11:51:02

Input Set : A:\ONV-044.01 SeqList.txt
Output Set: N:\CRF3\11282000\H900220C.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
C--> 6 (i) APPLICANT: Miao, Ningning
7 Wang, Monica
8 Mahanthappa, Nagesh K.
9 Pang, Kevin
10 Jin, Ping
12 (ii) TITLE OF INVENTION: Method of Treating Dopaminergic and
13 GABA-nergic Disorders
15 (iii) NUMBER OF SEQUENCES: 32
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
19 (B) STREET: ONE POST OFFICE SQUARE
20 (C) CITY: Boston
21 (D) STATE: MA
22 (E) COUNTRY: USA
23 (F) ZIP: 02109
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: AscII (text)
31 (vi) CURRENT APPLICATION DATA:
C--> 32 (A) APPLICATION NUMBER: US/08/900,220C
C--> 33 (B) FILING DATE: 24-Jul-1997
34 (C) CLASSIFICATION:
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Vincent, Matthew P.
38 (B) REGISTRATION NUMBER: 36,709
39 (C) REFERENCE/DOCKET NUMBER: ONV-044.01
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (617) 832-1000
43 (B) TELEFAX: (617) 832-7000
46 (2) INFORMATION FOR SEQ ID NO: 1:
47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 1277 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: both
51 (D) TOPOLOGY: linear
53 (ii) MOLECULE TYPE: cDNA
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..1275
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC
62 Met Val Glu Met Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
63 1 5 10 15

ENTERED

see p.5

RECEIVED

DEC 15 2000

TECH CENTER 1600/2900

#31

11/3

48

RAW SEQUENCE LISTING

DATE: 11/28/2000

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Input Set : A:\ONV-044.01 SeqList.txt

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | TGC | GCT | CTT | TTA | GTC | TCC | TCT | GGG | CTG | ACT | TGT | GGA | CCA | GGC | AGG | GGC | 96 |
| 66 | Cys | Ala | Leu | Leu | Val | Ser | Ser | Gly | Leu | Thr | Cys | Gly | Pro | Gly | Arg | Gly | |
| 67 | | | 20 | | | | | | 25 | | | | | 30 | | | |
| 69 | ATT | GGA | AAA | AGG | AGG | CAC | CCC | AAA | AAG | CTG | ACC | CCG | TTA | GCC | TAT | AAG | 144 |
| 70 | Ile | Gly | Lys | Arg | Arg | His | Pro | Lys | Lys | Leu | Thr | Pro | Leu | Ala | Tyr | Lys | |
| 71 | | | 35 | | | | | | 40 | | | | | 45 | | | |
| 73 | CAG | TTT | ATT | CCC | AAT | GTG | GCA | GAG | AAG | ACC | CTA | GGG | GCC | AGT | GGA | AGA | 192 |
| 74 | Gln | Phe | Ile | Pro | Asn | Val | Ala | Glu | Lys | Thr | Leu | Gly | Ala | Ser | Gly | Arg | |
| 75 | | | 50 | | | | | | 55 | | | | | 60 | | | |
| 77 | TAT | GAA | GGG | AAG | ATC | ACA | AGA | AAC | TCC | GAG | AGA | TTT | AAA | GAA | CTA | ACC | 240 |
| 78 | Tyr | Glu | Gly | Lys | Ile | Thr | Arg | Asn | Ser | Glu | Arg | Phe | Lys | Glu | Leu | Thr | |
| 79 | | | 65 | | | | | | 70 | | | | | 75 | | 80 | |
| 81 | CCA | AAT | TAC | AAC | CCT | GAC | ATT | ATT | TTT | AAG | GAT | GAA | GAG | AAC | ACG | GGA | 288 |
| 82 | Pro | Asn | Tyr | Asn | Pro | Asp | Ile | Ile | Phe | Lys | Asp | Glu | Glu | Asn | Thr | Gly | |
| 83 | | | | 85 | | | | | | 90 | | | | 95 | | | |
| 85 | GCT | GAC | AGA | CTG | ATG | ACT | CAG | CGC | TGC | AAG | GAC | AAG | CTG | AAT | GCC | CTG | 336 |
| 86 | Ala | Asp | Arg | Leu | Met | Thr | Gln | Arg | Cys | Lys | Asp | Lys | Leu | Asn | Ala | Leu | |
| 87 | | | 100 | | | | | | 105 | | | | | 110 | | | |
| 89 | GCG | ATC | TCG | GTG | ATG | AAC | CAG | TGG | CCC | GGG | GTG | AAG | CTG | CGG | GTG | ACC | 384 |
| 90 | Ala | Ile | Ser | Val | Met | Asn | Gln | Trp | Pro | Gly | Val | Lys | Leu | Arg | Val | Thr | |
| 91 | | | 115 | | | | | | 120 | | | | | 125 | | | |
| 93 | GAG | GGC | TGG | GAC | GAG | GAT | GGC | CAT | CAC | TCC | GAG | GAA | TCG | CTG | CAC | TAC | 432 |
| 94 | Glu | Gly | Trp | Asp | Glu | Asp | Gly | His | His | Ser | Glu | Glu | Ser | Leu | His | Tyr | |
| 95 | | | 130 | | | | | | 135 | | | | | 140 | | | |
| 97 | GAG | GGT | CGC | GCC | GTG | GAC | ATC | ACC | ACG | TCG | GAT | CGG | GAC | CGC | AGC | AAG | 480 |
| 98 | Glu | Gly | Arg | Ala | Val | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | Ser | Lys | |
| 99 | 145 | | | | | 150 | | | | 155 | | | | 160 | | | |
| 101 | TAC | GGA | ATG | CTG | GCC | CGC | CTC | GCC | GTC | GAG | GCC | GGC | TTC | GAC | TGG | GTC | 528 |
| 102 | Tyr | Gly | Met | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | |
| 103 | | | | 165 | | | | | | 170 | | | | 175 | | | |
| 105 | TAC | TAC | GAG | TCC | AAG | GCG | CAC | ATC | CAC | TGC | TCC | GTC | AAA | GCA | GAA | AAC | 576 |
| 106 | Tyr | Tyr | Glu | Ser | Lys | Ala | His | Ile | His | Cys | Ser | Val | Lys | Ala | Glu | Asn | |
| 107 | | | | 180 | | | | | | 185 | | | | 190 | | | |
| 109 | TCA | GTG | GCA | GCG | AAA | TCA | GGA | GGC | TGC | TTC | CCT | GGC | TCA | GCC | ACA | GTG | 624 |
| 110 | Ser | Val | Ala | Ala | Lys | Ser | Gly | Gly | Cys | Phe | Pro | Gly | Ser | Ala | Thr | Val | |
| 111 | | | 195 | | | | | | 200 | | | | | 205 | | | |
| 113 | CAC | CTG | GAG | CAT | GGA | GGC | ACC | AAG | CTG | GTG | AAG | GAC | CTG | AGC | CCT | GGG | 672 |
| 114 | His | Leu | Glu | His | Gly | Gly | Thr | Lys | Leu | Val | Lys | Asp | Leu | Ser | Pro | Gly | |
| 115 | | | 210 | | | | | | 215 | | | | | 220 | | | |
| 117 | GAC | CGC | GTG | CTG | GCT | GCT | GAC | GCG | GAC | GGC | CGG | CTG | CTC | TAC | AGT | GAC | 720 |
| 118 | Asp | Arg | Val | Leu | Ala | Ala | Asp | Ala | Asp | Gly | Arg | Leu | Leu | Tyr | Ser | Asp | |
| 119 | 225 | | | | | 230 | | | | 235 | | | | 240 | | | |
| 121 | TTC | CTC | ACC | TTC | CTC | GAC | CGG | ATG | GAC | AGC | TCC | CGA | AAG | CTC | TTC | TAC | 768 |
| 122 | Phe | Leu | Thr | Phe | Leu | Asp | Arg | Met | Asp | Ser | Ser | Arg | Lys | Leu | Phe | Tyr | |
| 123 | | | | 245 | | | | | | 250 | | | | 255 | | | |
| 125 | GTC | ATC | GAG | ACG | CGG | CAG | CCC | CGG | GCC | CGG | CTG | CTA | CTG | ACG | GCG | GCC | 816 |
| 126 | Val | Ile | Glu | Thr | Arg | Gln | Pro | Arg | Ala | Arg | Leu | Leu | Leu | Thr | Ala | Ala | |
| 127 | | | 260 | | | | | | 265 | | | | | 270 | | | |
| 129 | CAC | CTG | CTC | TTT | GTG | GCC | CCC | CAG | CAC | AAC | CAG | TCG | GAG | GCC | ACA | GGG | 864 |

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```

130 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
131      275      280      285
133 TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA      912
134 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
135      290      295      300
137 CCT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT      960
138 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
139 305      310      315
141 GTC CAC AGC GTC TCA TTG CGG GAG GAG GCC TCC GGA GCC TAC GCC CCA      1008
142 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
143      325      330      335
145 CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC      1056
146 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
147      340      345      350
149 TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA      1104
150 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
151      355      360      365
153 TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC      1152
154 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
155      370      375      380
157 ATC CCT ACT GCC GCC ACC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG      1200
158 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
159 385      390      395      400
160 CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT      1248
161 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
162      405      410      415
163 CCG CTG GCC ATG GTG GCA CCG GCC AGC TG      1277
164 Pro Leu Gly Met Val Ala Pro Ala Ser
165      420      425
168 (2) INFORMATION FOR SEQ ID NO: 2:
170 (i) SEQUENCE CHARACTERISTICS:
171 (A) LENGTH: 1190 base pairs
172 (B) TYPE: nucleic acid
173 (C) STRANDEDNESS: both
174 (D) TOPOLOGY: linear
176 (ii) MOLECULE TYPE: cDNA
178 (ix) FEATURE:
179 (A) NAME/KEY: CDS
180 (B) LOCATION: 1..1191
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
184 ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG      48
185 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
186 1      5      10      15
188 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG      96
189 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
190      20      25      30
192 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT      144
193 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
194      35      40      45

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 196 | GTG | CCC | AGT | ATG | CCC | GAG | CGG | ACC | CTG | GGC | GCG | AGT | GGG | CCA | GCG | GAG | 192 |
| 197 | Val | Pro | Ser | Met | Pro | Glu | Arg | Thr | Leu | Gly | Ala | Ser | Gly | Pro | Ala | Glu | |
| 198 | | 50 | | | | | 55 | | | | | 60 | | | | | |
| 200 | GGG | AGG | GTA | ACA | AGG | GGG | TCG | GAG | CGC | TTC | CGG | GAC | CTC | GTA | CCC | AAC | 240 |
| 201 | Gly | Arg | Val | Thr | Arg | Gly | Ser | Glu | Arg | Phe | Arg | Asp | Leu | Val | Pro | Asn | |
| 202 | 65 | | | | | 70 | | | | | 75 | | | | 80 | | |
| 204 | TAC | AAC | CCC | GAC | ATA | ATC | TTC | AAG | GAT | GAG | GAG | AAC | AGC | GGC | GCA | GAC | 288 |
| 205 | Tyr | Asn | Pro | Asp | Ile | Ile | Phe | Lys | Asp | Glu | Glu | Asn | Ser | Gly | Ala | Asp | |
| 206 | | | | | 85 | | | | | 90 | | | | | 95 | | |
| 208 | CGC | CTG | ATG | ACA | GAG | CGT | TGC | AAA | GAG | CGG | GTG | AAC | GCT | CTA | GCC | ATC | 336 |
| 209 | Arg | Leu | Met | Thr | Glu | Arg | Cys | Lys | Glu | Arg | Val | Asn | Ala | Leu | Ala | Ile | |
| 210 | | | 100 | | | | | | 105 | | | | | 110 | | | |
| 212 | GCG | GTG | ATG | AAC | ATG | TGG | CCC | GGA | GTA | CGC | CTA | CGT | GTG | ACT | GAA | GGC | 384 |
| 213 | Ala | Val | Met | Asn | Met | Trp | Pro | Gly | Val | Arg | Leu | Arg | Val | Thr | Glu | Gly | |
| 214 | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 216 | TGG | GAC | GAG | GAC | GGC | CAC | CAC | GCA | CAG | GAT | TCA | CTC | CAC | TAC | GAA | GGC | 432 |
| 217 | Trp | Asp | Glu | Asp | Gly | His | His | Ala | Gln | Asp | Ser | Leu | His | Tyr | Glu | Gly | |
| 218 | | 130 | | | | 135 | | | | | | 140 | | | | | |
| 220 | CGT | GCC | TTG | GAC | ATC | ACC | ACG | TCT | GAC | CGT | GAC | CGT | AAT | AAG | TAT | GGT | 480 |
| 221 | Arg | Ala | Leu | Asp | Ile | Thr | Thr | Ser | Asp | Arg | Asp | Arg | Asn | Lys | Tyr | Gly | |
| 222 | 145 | | | | | 150 | | | | | 155 | | | | 160 | | |
| 224 | TTG | TTG | GCG | CGC | CTA | GCT | GTG | GAA | GCC | GGA | TTC | GAC | TGG | GTC | TAC | TAC | 528 |
| 225 | Leu | Leu | Ala | Arg | Leu | Ala | Val | Glu | Ala | Gly | Phe | Asp | Trp | Val | Tyr | Tyr | |
| 226 | | | | 165 | | | | | | 170 | | | | 175 | | | |
| 228 | GAG | TCC | CGC | AAC | CAC | ATC | CAC | GTA | TCG | GTC | AAA | GCT | GAT | AAC | TCA | CTG | 576 |
| 229 | Glu | Ser | Arg | Asn | His | Ile | His | Val | Ser | Val | Lys | Ala | Asp | Asn | Ser | Leu | |
| 230 | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 232 | GCG | GTC | CGA | GCC | GGA | GGC | TGC | TTT | CCG | GGA | AAT | GCC | ACG | GTG | CGC | TTG | 624 |
| 233 | Ala | Val | Arg | Ala | Gly | Gly | Cys | Phe | Pro | Gly | Asn | Ala | Thr | Val | Arg | Leu | |
| 234 | | 195 | | | | | 200 | | | | | 205 | | | | | |
| 236 | CGG | AGC | GGC | GAA | CGG | AAG | GGG | CTG | AGG | GAA | CTA | CAT | CGT | GGT | GAC | TGG | 672 |
| 237 | Arg | Ser | Gly | Glu | Arg | Lys | Gly | Leu | Arg | Glu | Leu | His | Arg | Gly | Asp | Trp | |
| 238 | | 210 | | | | | 215 | | | | | 220 | | | | | |
| 240 | GTA | CTG | GCC | GCT | GAT | GCA | GCG | GGC | CGA | GTG | GTA | CCC | ACG | CCA | GTG | CTG | 720 |
| 241 | Val | Leu | Ala | Ala | Asp | Ala | Ala | Gly | Arg | Val | Val | Pro | Thr | Pro | Val | Leu | |
| 242 | 225 | | | | | 230 | | | | | | 235 | | | 240 | | |
| 244 | CTC | TTC | CTG | GAC | CGG | GAT | CTG | CAG | CGC | CGC | GCC | TCG | TTC | GTG | GCT | GTG | 768 |
| 245 | Leu | Phe | Leu | Asp | Arg | Asp | Leu | Gln | Arg | Arg | Ala | Ser | Phe | Val | Ala | Val | |
| 246 | | | | 245 | | | | | | 250 | | | | 255 | | | |
| 248 | GAG | ACC | GAG | CGG | CCT | CCG | CGC | AAA | CTG | TTG | CTC | ACA | CCC | TGG | CAT | CTG | 816 |
| 249 | Glu | Thr | Glu | Arg | Pro | Pro | Arg | Lys | Leu | Leu | Leu | Thr | Pro | Trp | His | Leu | |
| 250 | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 252 | GTG | TTC | GCT | GCT | CGC | GGG | CCA | GCG | CCT | GCT | CCA | GGT | GAC | TTT | GCA | CCG | 864 |
| 253 | Val | Phe | Ala | Ala | Arg | Gly | Pro | Ala | Pro | Ala | Pro | Gly | Asp | Phe | Ala | Pro | |
| 254 | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 256 | GTG | TTC | GCG | CGC | CGC | TTA | CGT | GCT | GGC | GAC | TCG | GTG | CTG | GCT | CCC | GGC | 912 |
| 257 | Val | Phe | Ala | Arg | Arg | Leu | Arg | Ala | Gly | Asp | Ser | Val | Leu | Ala | Pro | Gly | |
| 258 | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 260 | GGG | GAC | GCG | CTC | CAG | CCG | GCG | CGC | GTA | GCC | CGC | GTG | GCG | CGC | GAG | GAA | 960 |

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261 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
262 305 310 315 320
264 GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC 1008
265 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
266 325 330 335
268 AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG 1056
269 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
270 340 345 350
271 GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT 1104
272 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
273 355 360 365
275 CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT 1152
276 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
277 370 375 380
279 CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG 1190
280 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
281 385 390 395
284 (2) INFORMATION FOR SEQ ID NO: 3:
286 (i) SEQUENCE CHARACTERISTICS:
287 (A) LENGTH: 1281 base pairs
288 (B) TYPE: nucleic acid
289 (C) STRANDEDNESS: both
290 (D) TOPOLOGY: linear
292 (ii) MOLECULE TYPE: cDNA
295 (ix) FEATURE:
296 (A) NAME/KEY: CDS
297 (B) LOCATION: 1..1233
299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
301 ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG 48
302 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
303 1 5 10 15
305 CTG CTG CTG CTT CTG GTG CCG GCG GCG GGC TGC GGG CCG GGC CGG 96
306 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
307 20 25 30
309 GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC 144
310 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
311 35 40 45
313 TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC 192
314 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
315 50 55 60
317 GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG 240
318 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
319 65 70 75 80
321 CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC 288
322 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
323 85 90 95
325 ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC 336
326 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
327 100 105 110

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← F.Y.I.

VERIFICATION SUMMARY

DATE: 11/28/2000

PATENT APPLICATION: US/08/900,220C

TIME: 11:51:03

Input Set : A:\ONV-044.01 SeqList.txt

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L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2347 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23, Value=[nucleic acid]
L:2363 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24, Value=[nucleic acid]
L:2378 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25, Value=[nucleic acid]
L:2409 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26, Value=[nucleic acid]
L:2424 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27, Value=[nucleic acid]
L:2439 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28, Value=[nucleic acid]
L:2453 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29, Value=[nucleic acid]
L:2467 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30, Value=[nucleic acid]
L:2481 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31, Value=[nucleic acid]
L:2495 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32, Value=[nucleic acid]